



IFWO

RAW SEQUENCE LISTING

DATE: 08/11/2004

PATENT APPLICATION: US/10/660,113

TIME: 11:04:46

Input Set : A:\36-001720US.ST25.txt

Output Set: N:\CRF4\08112004\J660113.raw

3 <110> APPLICANT: IRM, LLC and Novartis Pharmaceuticals Corporation
 4 Shah, Kavita
 5 Vincent, Fabien
 6 Cueto, Maria A
 8 <120> TITLE OF INVENTION: HIGHLY SPECIFIC MODULATORS OF GTPASES FOR TARGET VALIDATION
 10 <130> FILE REFERENCE: 36-001720US
 12 <140> CURRENT APPLICATION NUMBER: US 10/660,113
 13 <141> CURRENT FILING DATE: 2003-09-10
 15 <160> NUMBER OF SEQ ID NOS: 52
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 189
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Homo sapiens
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 27 1 5 10 15
 30 Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
 31 20 25 30
 34 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
 35 35 40 45
 38 Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
 39 50 55 60
 42 Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
 43 65 70 75 80
 46 Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
 47 85 90 95
 50 Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
 51 100 105 110
 54 Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
 55 115 120 125
 58 Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
 59 130 135 140
 62 Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
 63 145 150 155 160
 66 Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu
 67 165 170 175
 70 Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
 71 180 185
 74 <210> SEQ ID NO: 2
 75 <211> LENGTH: 189
 76 <212> TYPE: PRT
 77 <213> ORGANISM: artificial

ENTERED

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79 <220> FEATURE:

80 <223> OTHER INFORMATION: mutant of H-Ras

82 <400> SEQUENCE: 2

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84 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
85 1          5          10          15
88 Ser Ala Ala Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
89          20          25          30
92 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
93          35          40          45
96 Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
97          50          55          60
100 Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
101 65          70          75          80
104 Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
105          85          90          95
108 Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
109          100          105          110
112 Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
113          115          120          125
116 Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
117          130          135          140
120 Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
121 145          150          155          160
124 Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu
125          165          170          175
128 Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
129          180          185

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132 <210> SEQ ID NO: 3

133 <211> LENGTH: 189

134 <212> TYPE: PRT

135 <213> ORGANISM: artificial

137 <220> FEATURE:

138 <223> OTHER INFORMATION: mutant of H-Ras

140 <400> SEQUENCE: 3

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142 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
143 1          5          10          15
146 Ser Ala Gly Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
147          20          25          30
150 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
151          35          40          45
154 Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
155          50          55          60
158 Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
159 65          70          75          80
162 Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
163          85          90          95
166 Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
167          100          105          110
170 Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg

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171          115          120          125
174 Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
175          130          135          140
178 Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
179 145          150          155          160
182 Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu
183          165          170          175
186 Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
187          180          185
190 <210> SEQ ID NO: 4
191 <211> LENGTH: 189
192 <212> TYPE: PRT
193 <213> ORGANISM: artificial
195 <220> FEATURE:
196 <223> OTHER INFORMATION: mutant of H-Ras
198 <400> SEQUENCE: 4
200 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
201 1          5          10          15
204 Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Ala Val Asp Glu Tyr
205          20          25          30
208 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
209          35          40          45
212 Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
213          50          55          60
216 Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
217 65          70          75          80
220 Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
221          85          90          95
224 Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
225          100          105          110
228 Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
229          115          120          125
232 Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
233          130          135          140
236 Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
237 145          150          155          160
240 Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu
241          165          170          175
244 Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
245          180          185
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 189
250 <212> TYPE: PRT
251 <213> ORGANISM: artificial
253 <220> FEATURE:
254 <223> OTHER INFORMATION: mutant of H-Ras
256 <400> SEQUENCE: 5
258 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
259 1          5          10          15

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262 Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Gly Val Asp Glu Tyr
263          20          25          30
266 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
267          35          40          45
270 Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
271          50          55          60
274 Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
275 65          70          75          80
278 Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
279          85          90          95
282 Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
283          100         105         110
286 Leu Val Gly Asn Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
287          115         120         125
290 Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
291          130         135         140
294 Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
295 145         150         155         160
298 Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu
299          165         170         175
302 Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
303          180         185
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307 <211> LENGTH: 189
308 <212> TYPE: PRT
309 <213> ORGANISM: artificial
311 <220> FEATURE:
312 <223> OTHER INFORMATION: mutant of H-Ras
314 <400> SEQUENCE: 6
316 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
317 1          5          10          15
320 Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
321          20          25          30
324 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
325          35          40          45
328 Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
329          50          55          60
332 Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
333 65          70          75          80
336 Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
337          85          90          95
340 Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
341          100         105         110
344 Leu Val Gly Ala Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
345          115         120         125
348 Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
349          130         135         140
352 Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
353 145         150         155         160

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356 Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu
357           165           170           175
360 Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
361           180           185
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365 <211> LENGTH: 189
366 <212> TYPE: PRT
367 <213> ORGANISM: artificial
369 <220> FEATURE:
370 <223> OTHER INFORMATION: mutant of H-Ras
372 <400> SEQUENCE: 7
374 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
375 1           5           10           15
378 Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
379           20           25           30
382 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
383           35           40           45
386 Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr
387           50           55           60
390 Ser Ala Met Arg Asp Gln Tyr Met Arg Thr Gly Glu Gly Phe Leu Cys
391 65           70           75           80
394 Val Phe Ala Ile Asn Asn Thr Lys Ser Phe Glu Asp Ile His Gln Tyr
395           85           90           95
398 Arg Glu Gln Ile Lys Arg Val Lys Asp Ser Asp Asp Val Pro Met Val
399           100          105          110
402 Leu Val Gly Gly Lys Cys Asp Leu Ala Ala Arg Thr Val Glu Ser Arg
403           115          120          125
406 Gln Ala Gln Asp Leu Ala Arg Ser Tyr Gly Ile Pro Tyr Ile Glu Thr
407           130          135          140
410 Ser Ala Lys Thr Arg Gln Gly Val Glu Asp Ala Phe Tyr Thr Leu Val
411 145           150          155          160
414 Arg Glu Ile Arg Gln His Lys Leu Arg Lys Leu Asn Pro Pro Asp Glu
415           165           170           175
418 Ser Gly Pro Gly Cys Met Ser Cys Lys Cys Val Leu Ser
419           180           185
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423 <211> LENGTH: 189
424 <212> TYPE: PRT
425 <213> ORGANISM: artificial
427 <220> FEATURE:
428 <223> OTHER INFORMATION: mutant of H-Ras
430 <400> SEQUENCE: 8
432 Met Thr Glu Tyr Lys Leu Val Val Val Gly Ala Gly Gly Val Gly Lys
433 1           5           10           15
436 Ser Ala Leu Thr Ile Gln Leu Ile Gln Asn His Phe Val Asp Glu Tyr
437           20           25           30
440 Asp Pro Thr Ile Glu Asp Ser Tyr Arg Lys Gln Val Val Ile Asp Gly
441           35           40           45
444 Glu Thr Cys Leu Leu Asp Ile Leu Asp Thr Ala Gly Gln Glu Glu Tyr

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RAW SEQUENCE LISTING ERROR SUMMARY

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Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,19,20,21,22,23,24,25,26,27,28,29

Seq#:30,31,32,33,34

VERIFICATION SUMMARY

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